AMENDMENTS TO THE SPECIFICATION

On page 1, after the title, please insert the following paragraph:

--PRIORITY CLAIM

This is a § 371 U.S. national stage of PCT/JP03/07004, filed June 3, 2003, and claims the benefit of Japanese Patent Application No. 2002-165437, filed June 6, 2002.--

Please replace the paragraph beginning on page 4, line 7, with the following paragraph:

--As an alternative to methods using viral vectors, *in vivo* gene transfer methods using liposomes together with viral outer membranes, or HVJ (hemagglutinating virus of Japan)-liposome-mediated gene transfer methods, have been developed (Science 243: 375-378 (1989); Anal. NY Acad. Sci. 772: 126-139 (1995)). *In vivo* gene transfers into various tissues, including the liver, kidney, vascular wall, heart, and brain, have been successfully accomplished using these methods (Gene Therapy 7: 417-427 (2000); Science 243: 375-378 (1989); Biochem. Biophys. Res. Commun. 186: 129-134 (1992); Proc. Natl. Acad. Sci. USA 90: 8474-8478 (1993); Am. J. Physiol. 271 (Regulatory Integrative Comp. Physiol. 40):R1212-R1220 (1996)).--

Please replace the paragraph beginning on page 5, line 29, with the following paragraph:

--In cerebral infarction, a cerebral edema occurs within a few hours of the onset of disease, and this condition continues for approximately one week after onset. Thereafter, the edema gradually decreases, but becomes fixed as an infarcted area within one to three months after onset. The cerebral edema causes the volume of the brain to increase. Since the brain is covered with a hard cranium, when the volume of the brain exceeds a certain limit due to the cerebral edema, rapid increase in tissue pressure and intra-cranial pressure results. Thus, brain damage worsens, and thereafter, the extent of the infarcted area is fixed (Inamura, K., Terashi, A. "Nippon Rinsho, Dai 51 Kan, CT, MRI Jidai no No-Sotchu Gaku, Jo-Kan (Nippon Rinsho, Vol. 51, Cerebral Apoplexy in the Age of CT and MRI, No. 1)" ~~Nippon Rinsho~~ Nihon Rinsho Sha, p231-239 (1993)). When an infarction occurs in a section of the brain, those functions carried by the affected part, such as cognition, perception, sense, and memory, are lost.--

Please replace the paragraph beginning on page 8, line 28, with the following paragraph:

--The term "HGF gene" as used in this invention refers to a nucleic acid molecule that can express an HGF (an HGF protein). Herein, the term "nucleic acid molecule" refers to molecules such as DNAs, RNAs, cDNAs, and mRNAs. Specifically, cDNAs that encode HGF are described in, for example, Nature 342: 440 (1989), Japanese Patent No. 2777678, and Biochem. Biophys. Res. Commun. 163: 967 (1989). The nucleotide sequences of cDNAs encoding HGF are described in the aforementioned literature, and are also registered in databases such as GenBank. Based on this sequence information, cDNAs of HGF can be cloned by using appropriate sequence segments as PCR primers, and by performing RT-PCR using, for example, mRNAs derived from the liver or leukocytes. One skilled in the art can readily perform such cloning by following fundamental texts, such as Molecular Cloning 2nd edition (Cold Spring Harbor Laboratory Press) (1989). Furthermore, by screening genomic DNA libraries, genomic DNAs can be isolated.--

Please replace the paragraph beginning on page 10, line 5, with the following paragraph:

-- The amino acid sequences of the proteins encoded by the nucleic acids isolated by the above-mentioned hybridization methods or PCR methods usually show high homology to conventionally known HGF proteins. The term "high homology" refers to a sequence homology of at least 50% or more, more preferably 70% or more, even more preferably 90% or more (for example, 95% or more). The sequence identity of amino acid sequences and nucleotide sequences can be determined using Karlin and Altschul's BLAST algorithm (Proc. Natl. Acad. Sci. USA 90: 5873-5877 (1993)). Programs such as BLASTN and BLASTX have been developed based on this algorithm (Altschul *et al.* J. Mol. Biol. 215: 403-410 (1990)). When nucleotide sequences are analyzed using BLASTN, based on BLAST, parameters are set, for example, at score = 100 and wordlength = 12. When amino acid sequences are analyzed by using BLASTX, based on BLAST, parameters are set, for example, at score = 50 and wordlength = 3. When using the BLAST and Gapped BLAST programs, the default parameters for the respective programs are used. Specific techniques for these analytical methods are well known (see, for example, the National Center for Biotechnology Information web site ~~http://www.ncbi.nlm.nih.gov~~).--